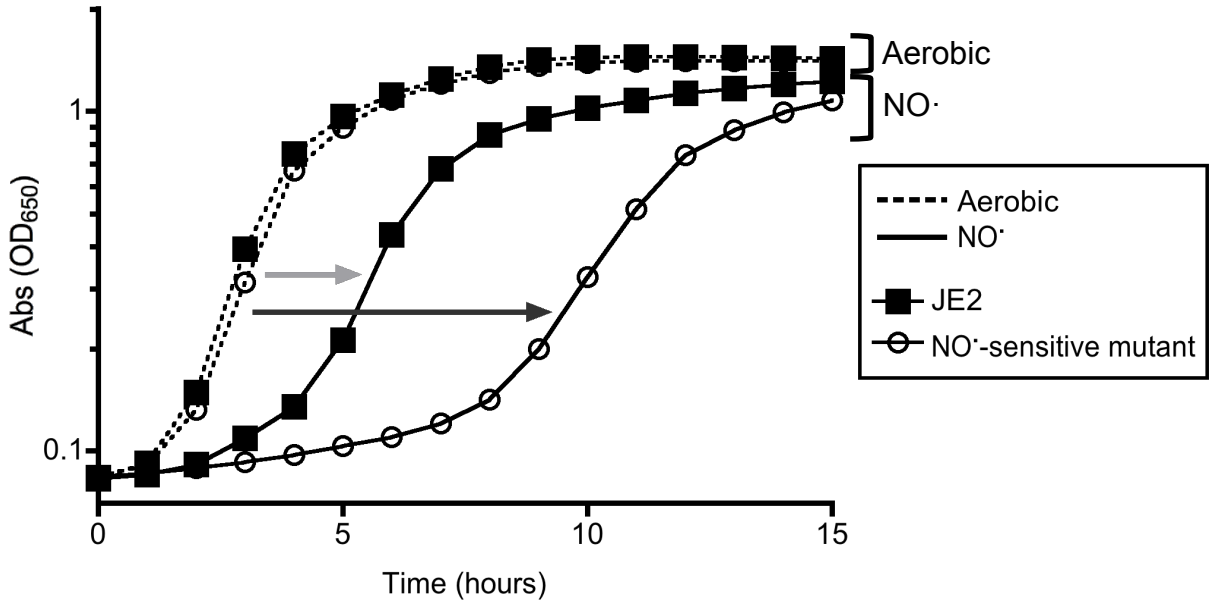

Figure S1. NO· addition at the time of inoculum extends the lag time of *S. aureus* JE2. *S. aureus* JE2 WT and mutants were grown in LB aerobically (dotted lines) and following exposure to 5mM DETA/NO at the time of inoculum (solid lines). NO· extends the lag time of WT JE2 by approximately 3-hrs (light gray arrow). Mutants with significantly extended lag times only when NO· is present (dark gray arrow) are NO·-sensitive

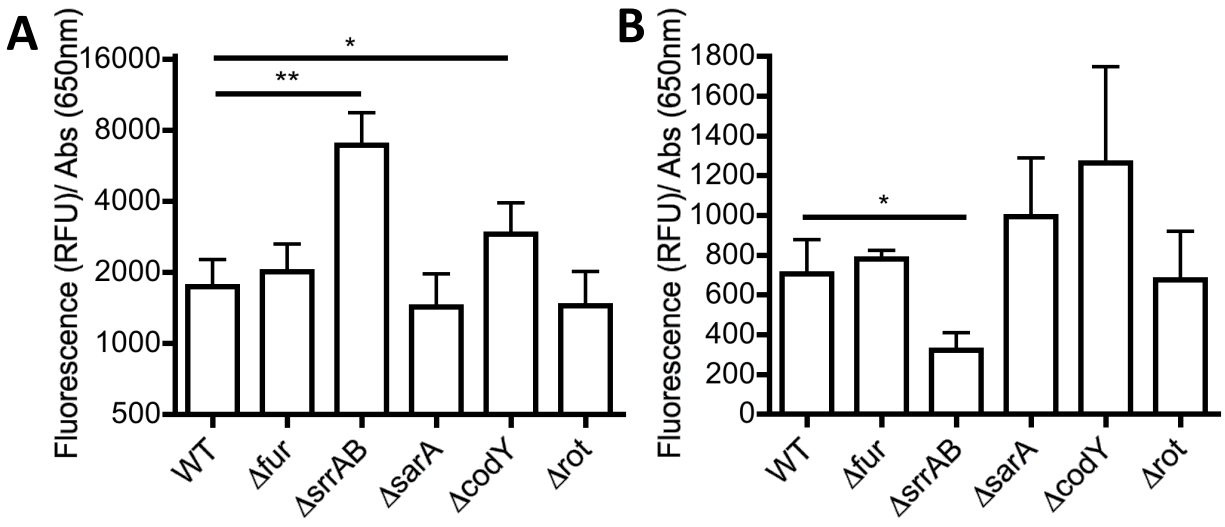

Figure S2. Expression of NO·-resistance genes *hmp* and *ldh1* in NO·-sensitive regulator mutants. Newman mutants harboring plasmids containing a transcriptional fusion of *gfp* to the promoter of either A) *ldh1* or B) *hmp* were grown in PNG and exposed to 2mM DETA/NO at an OD_{650} of 0.2. Shown is the peak value of relative fluorescence units (RFU) per OD_{650} of NO·-exposed cells minus the RFU/OD_{650} of aerobically grown cells. (n=3, error bars show SEM). Significance was calculated using a Student's two-sided t test (*, $P \leq 0.05$; **, $P \leq 0.01$).

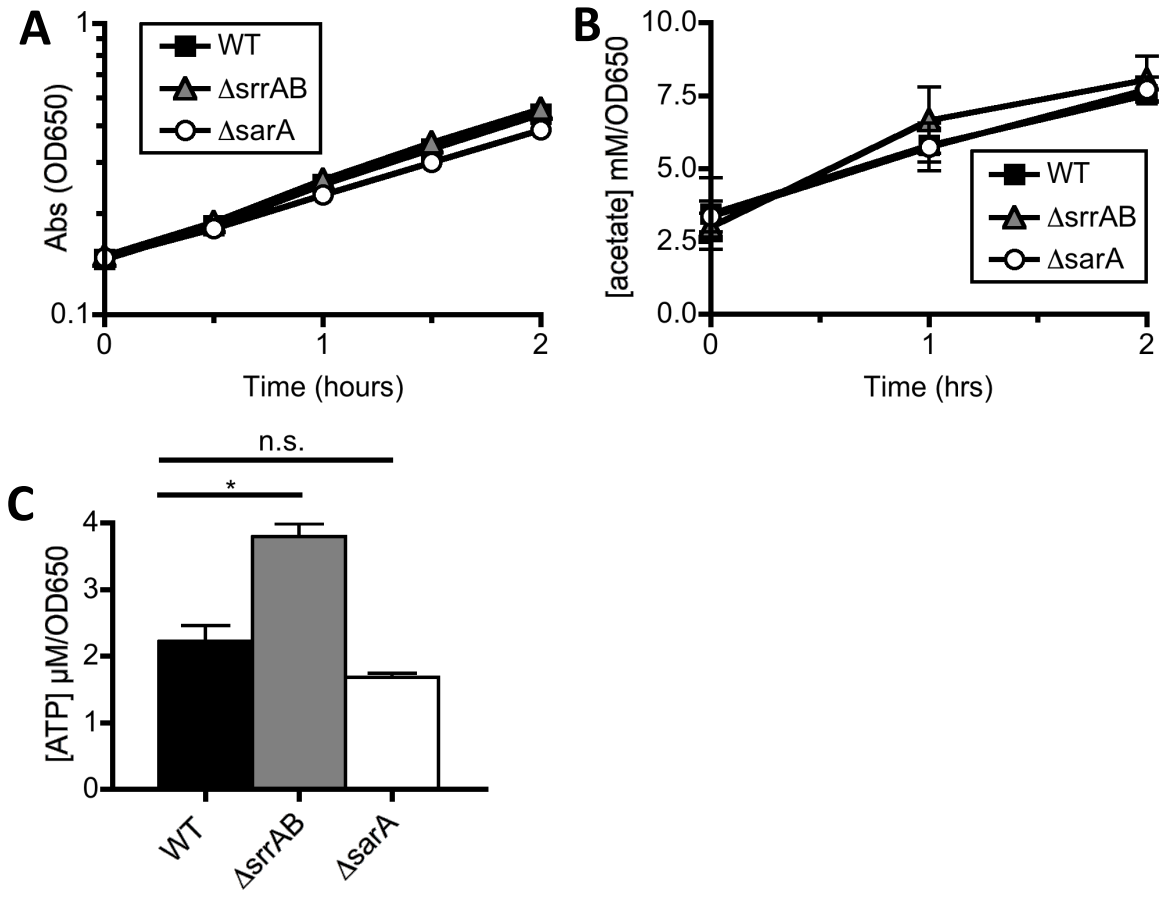

Figure S3. Δs*rrAB* and Δ*sarA* mutants exhibit normal acetogenesis and ATP levels during aerobic growth. A) Growth, (B) acetate production, and (C) ATP levels of *S. aureus* COL WT, Δ*srrAB,* and Δ*sarA* during aerobic growth in PNG (n=3). Significance was calculated using a two-sided Student's t-test ($P \leq 0.05$).

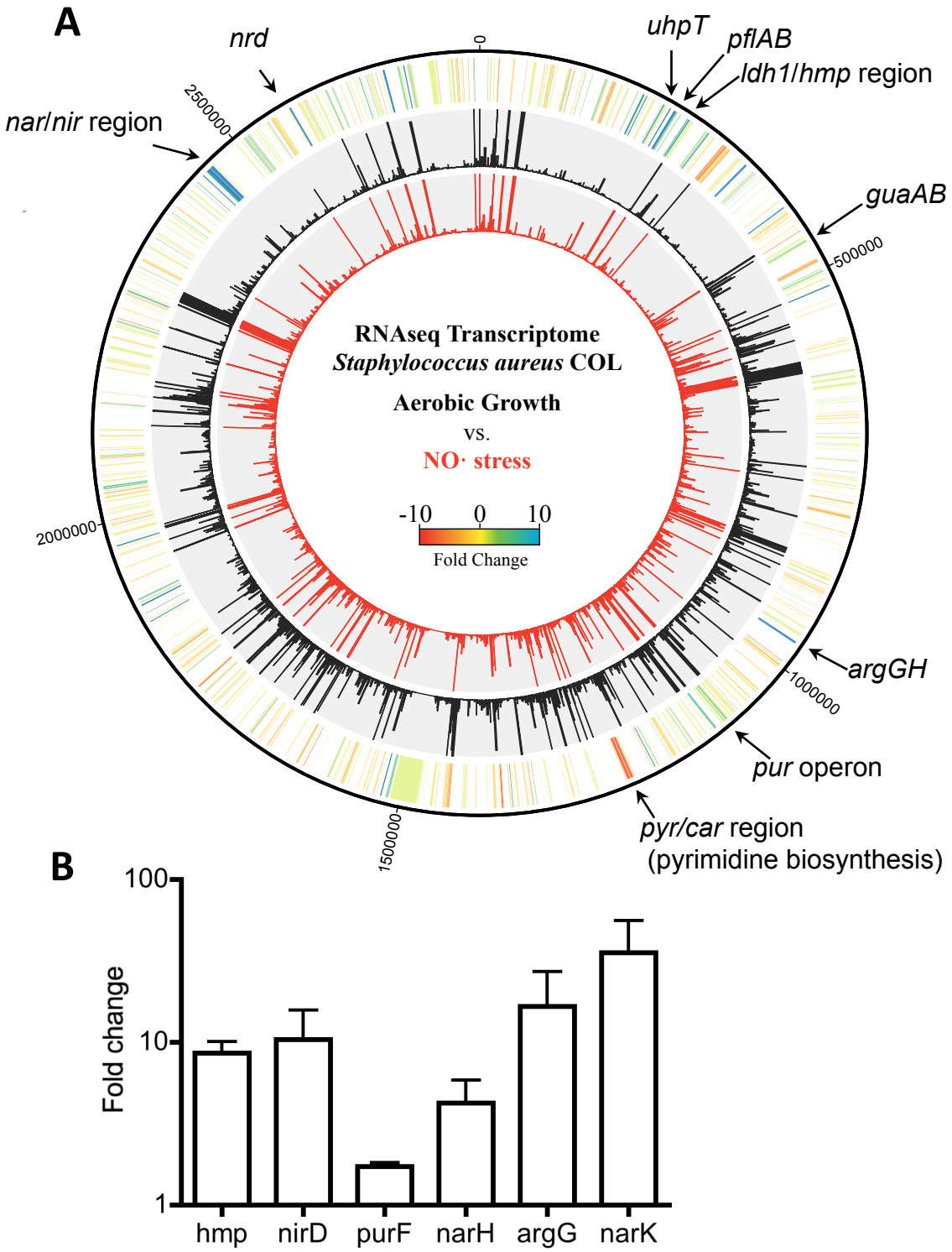

Figure S4. NO· induces a massive transcriptional response in *S. aureus* COL. (A) Genomic map showing transcription profiles of *S. aureus* COL grown in PNG either aerobically (middle black circle) or for 1-hr in the presence of 4mM DETA/NO (inner red circle). The outer yellow circle is a heat map depicting fold change differences in expression for the NO· exposed versus aerobically grown cells. (B) qRT-PCR data verifying the NO· responsiveness of a subset of genes identified as NO· inducible by RNA-Seq. Graph depicts the fold change in expression levels for NO·-exposed cells compared to cells grown aerobically (n=3, error bars show SEM).

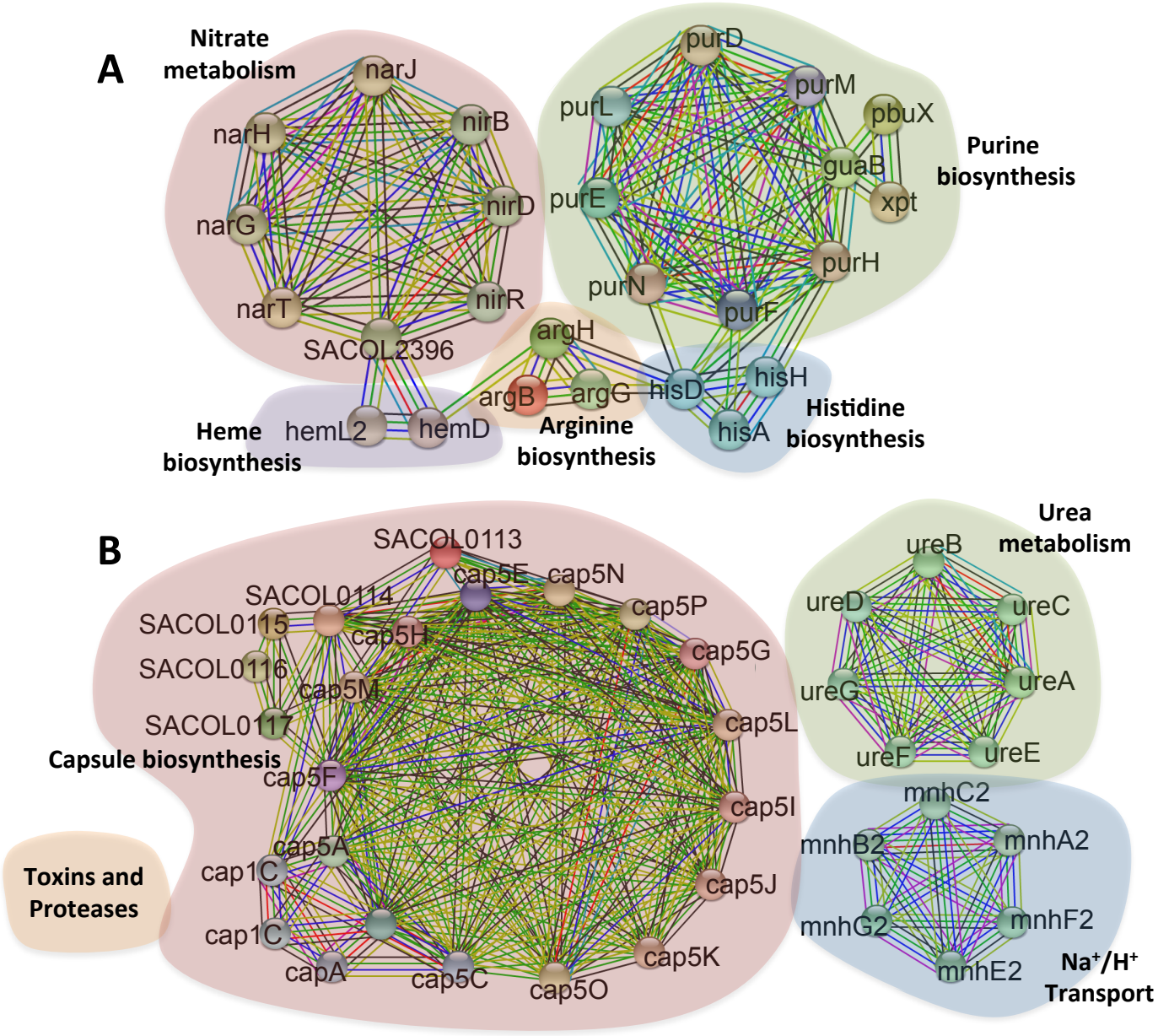

Figure S5. Associations among genes identified as having differential expression in the Δ*sarA* mutant compared to WT following NO·-exposure. Genes that were (A) underexpressed (<2-fold) or (B) overexpressed (>2-fold) in the NO·-exposed Δ*sar*A mutant compared to NO·-exposed WT were examined for gene/protein associations using the Search Tool for the Retrieval of Interacting Genes/Proteins (STRING) v10, high confidence setting. Each line represents a different association between genes. For clarity, only the most prominent clusters of predicted gene/protein associations are shown.

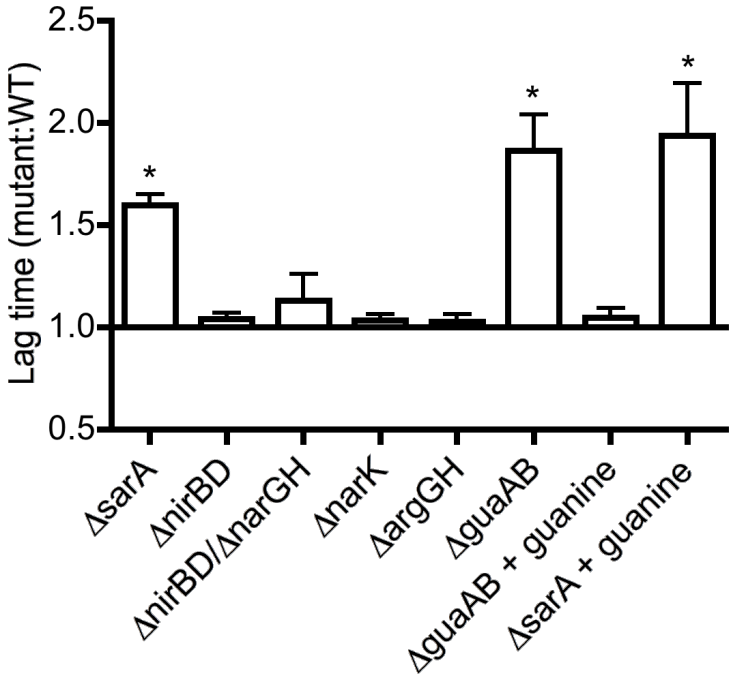

Figure S6. Select genes that are under-expressed in the NO·-exposed Δ*sarA* mutant are not individually required for NO· resistance. *S. aureus* Newman mutants were grown in LBGT media with or without the addition of 5mM DETA/NO at the time of inoculum. Lag time (time to OD_{650} 0.2) for each NO·-exposed strain was normalized to its aerobic lag time. Graphs depict the ratio of mutant to WT lag times (n=3, error bars show SEM). Significance was calculated using a two-sided Student's t-test to compare each mutant lag time to WT lag time (*, $P \leq 0.05$).